

CHAPTER 15

METAPOPULATIONS and FRAGMENTATION

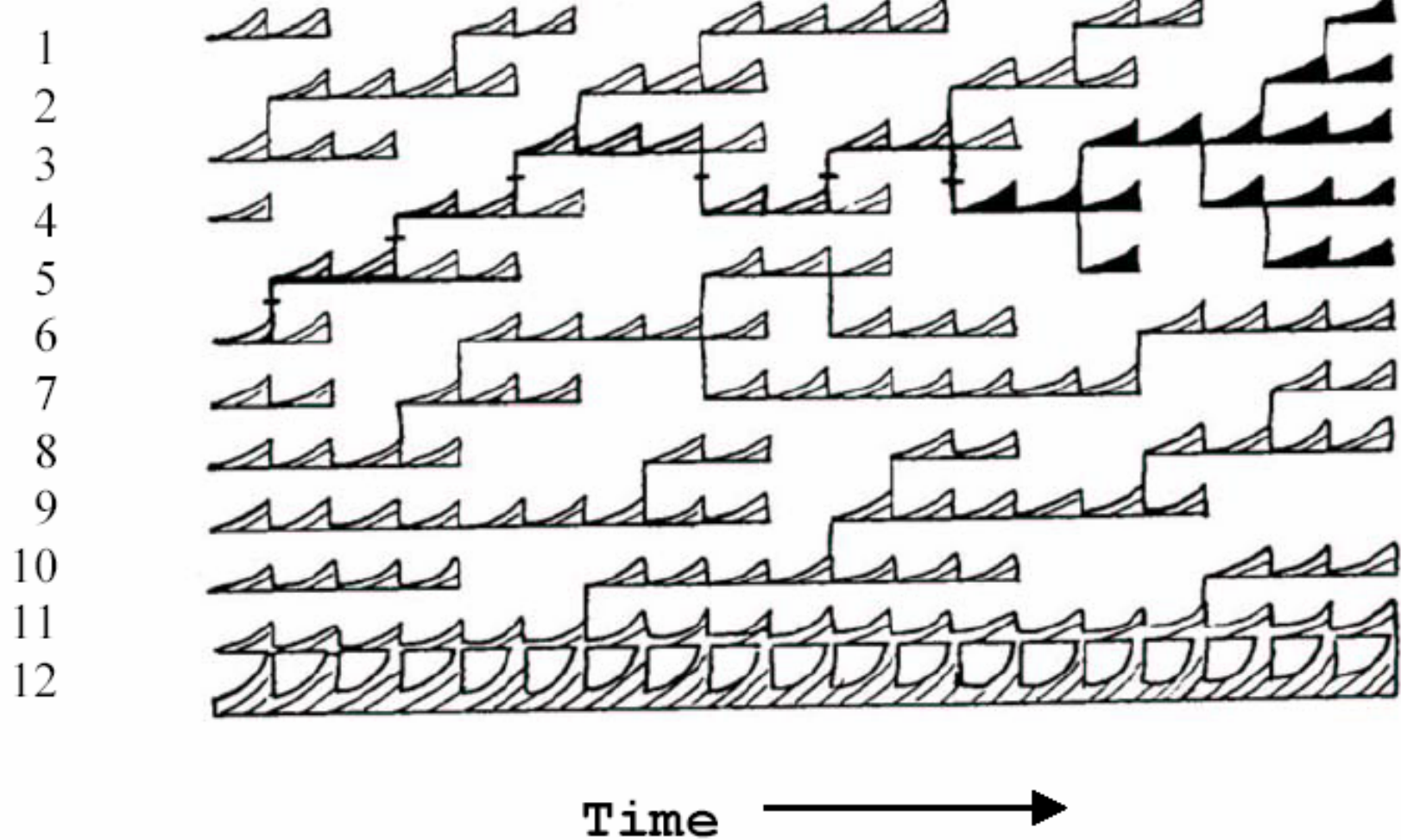
Theoretical results have shown that a pattern of local extinction and recolonization can have significant consequences for the genetic structure of subdivided populations; consequences that are relevant to issues in both evolutionary and conservation biology.

David McCauley (1991)

Metapopulation: collection of subpopulations, each of which occupies a separate patch of a subdivided habitat.

GENETICS AND POPULATION VIABILITY

- (1) Inbreeding depression
- (2) Loss of genetic and phenotypic variability
- (3) Loss of evolutionary potential
- (4) Effects of mtDNA
- (5) Mutational meltdown



An important case arises where local populations are liable to frequent extinction, with restoration from the progeny of a few stray immigrants. In such regions the line of continuity of large populations may have passed repeatedly through extremely small numbers even though the species has at all times included countless millions of individuals in its range as a whole.

Sewall Wright (1940)

Richard Levins (1970) introduced the term metapopulation to describe a population of populations that occupy a series of similar habitat patches isolated by unsuitable habitat.

Each local population has probability of extinction (e) during a time interval. Empty patches are subject to recolonization with probability (c).

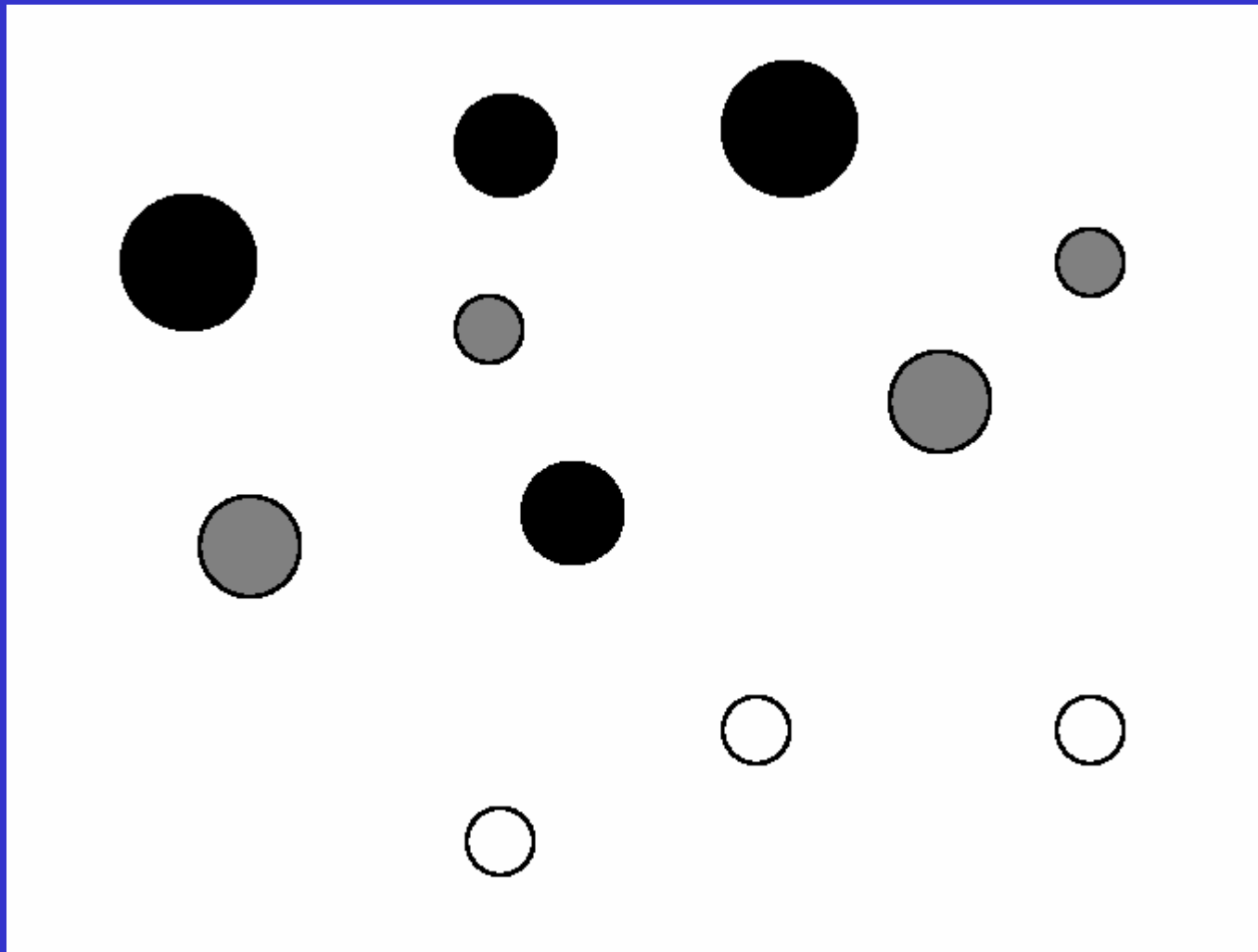
“Metapopulation dynamics” are a balance between extinction and recolonization so that at any particular time some patches are occupied and some are extinct.

e = probability of extinction

c = probability of colonization

p = proportion of patches occupied

$$p^* = \frac{c}{c + e}$$



Metapopulation dynamics:

Size (e & N_e) and distance (c & m)

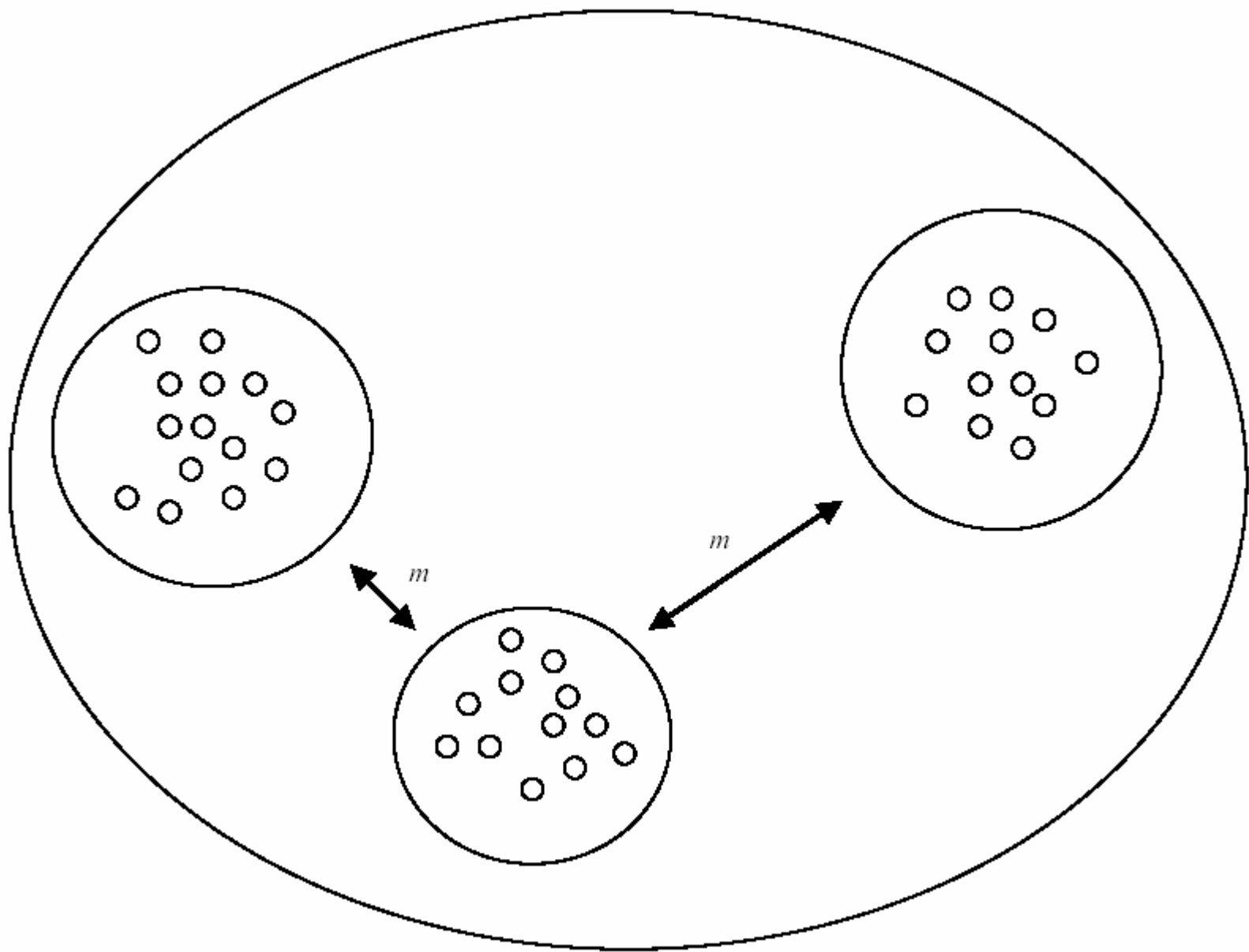
Importance of scale (geographical & temporal)

The LOCAL SCALE is the scale at which individuals move and interact with one another in their course of routine feeding and breeding activities.

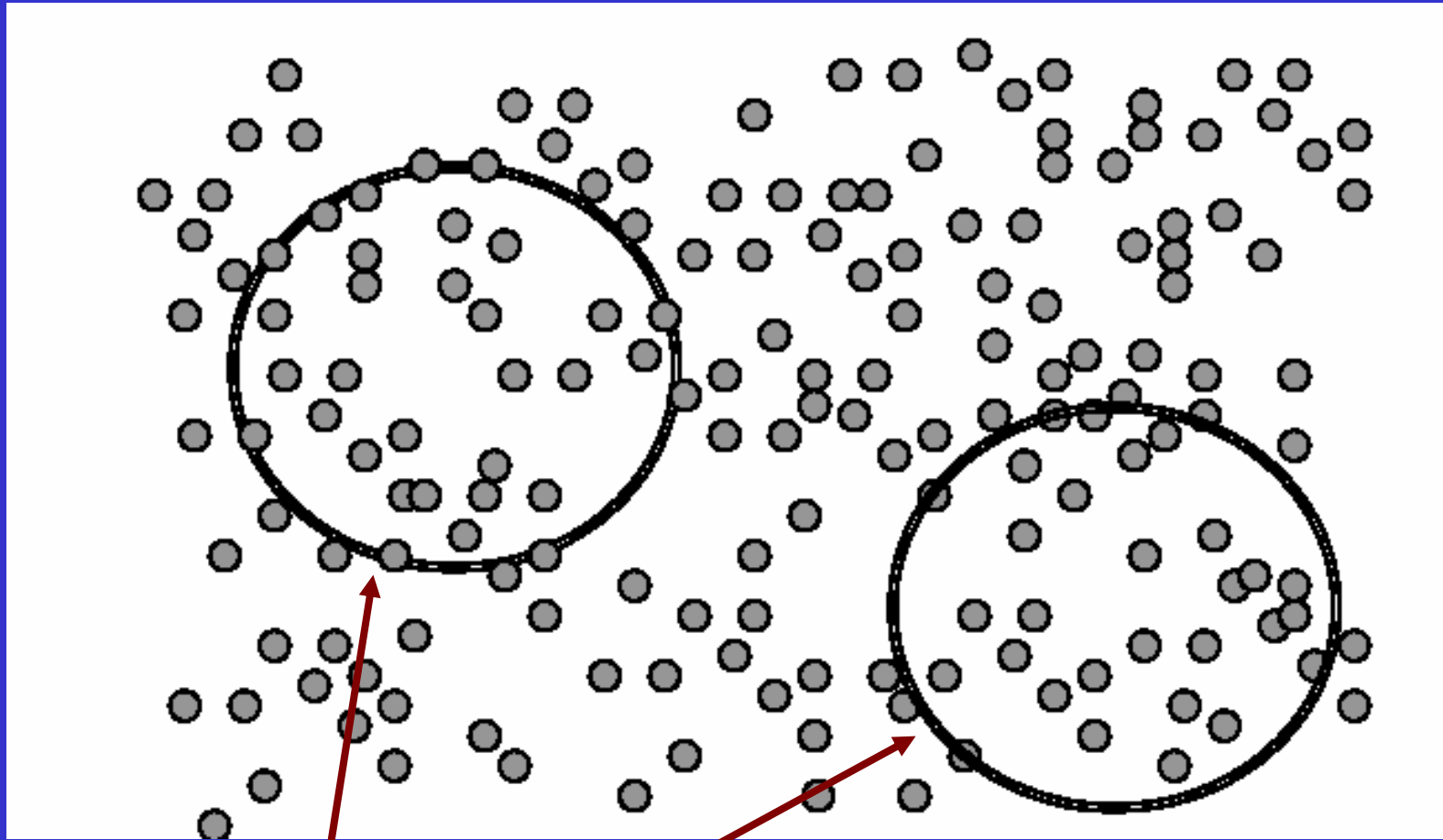
The METAPOPOPULATION SCALE is the scale at which individuals infrequently move from one local population to another, typically across habitat that is unsuitable for their feeding and breeding activities.

The SPECIES SCALE is the entire geographical range of a species; individuals typically have no possibility of moving to most parts of the range. Metapopulations on opposite ends of the range of a species do not exchange individuals, but they remain part of the same genetic species because of movement among intermediate metapopulations.

Effective population size (N_e)



Continuous Distribution Model (Isolation-by-distance)



neighborhoods

Who are the people in *your* neighborhood?

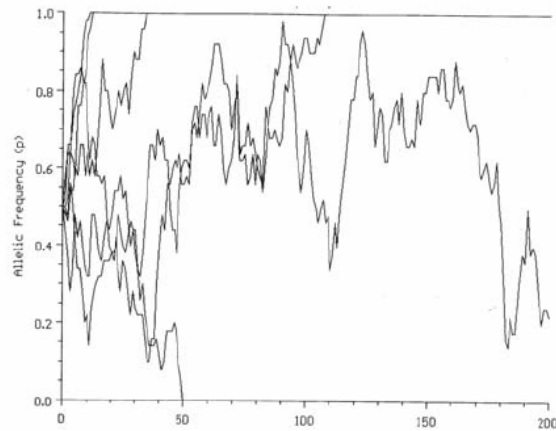


Effective population size (N_e)

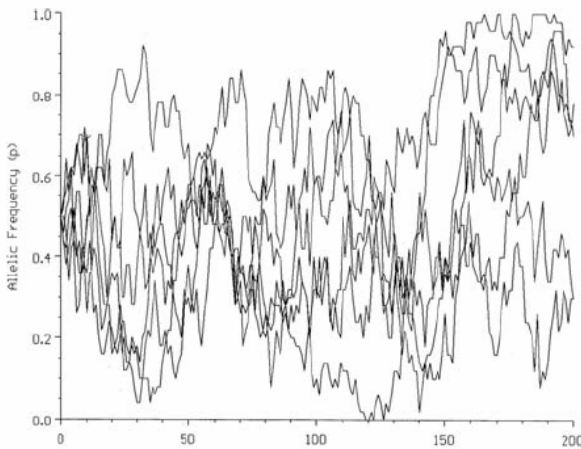
Effective population size is a measure of the rate of loss of heterozygosity over time. The short-term effective population size is related to the decline of the expected average heterozygosity within subpopulations (H_S). The long-term effective population size is related to the decline of the expected heterozygosity if the entire metapopulation were panmictic (H_T).

$$N_e (\text{local}) = 25$$

$$N_T = 6 \times 25 = 150$$



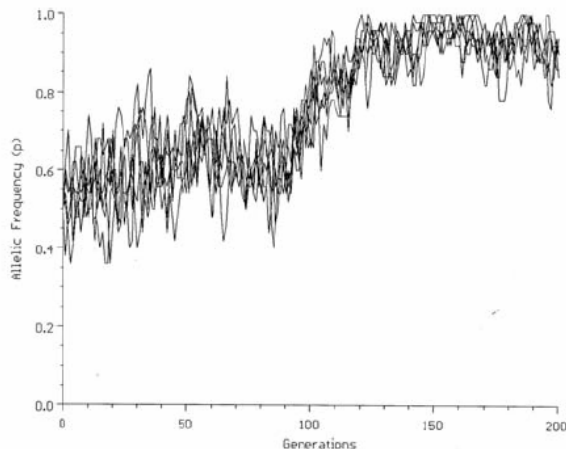
$$mN = 0$$



$$mN = 1$$

$$H_T = H_S + H_B$$

$$F_{ST} = H_B / H_T$$



$$mN = 10$$

Long-term Population Viability: $N_e \geq 500 - 1,000$

The LOCAL SCALE is the scale at which individuals move and interact with one another in their course of routine feeding and breeding activities.

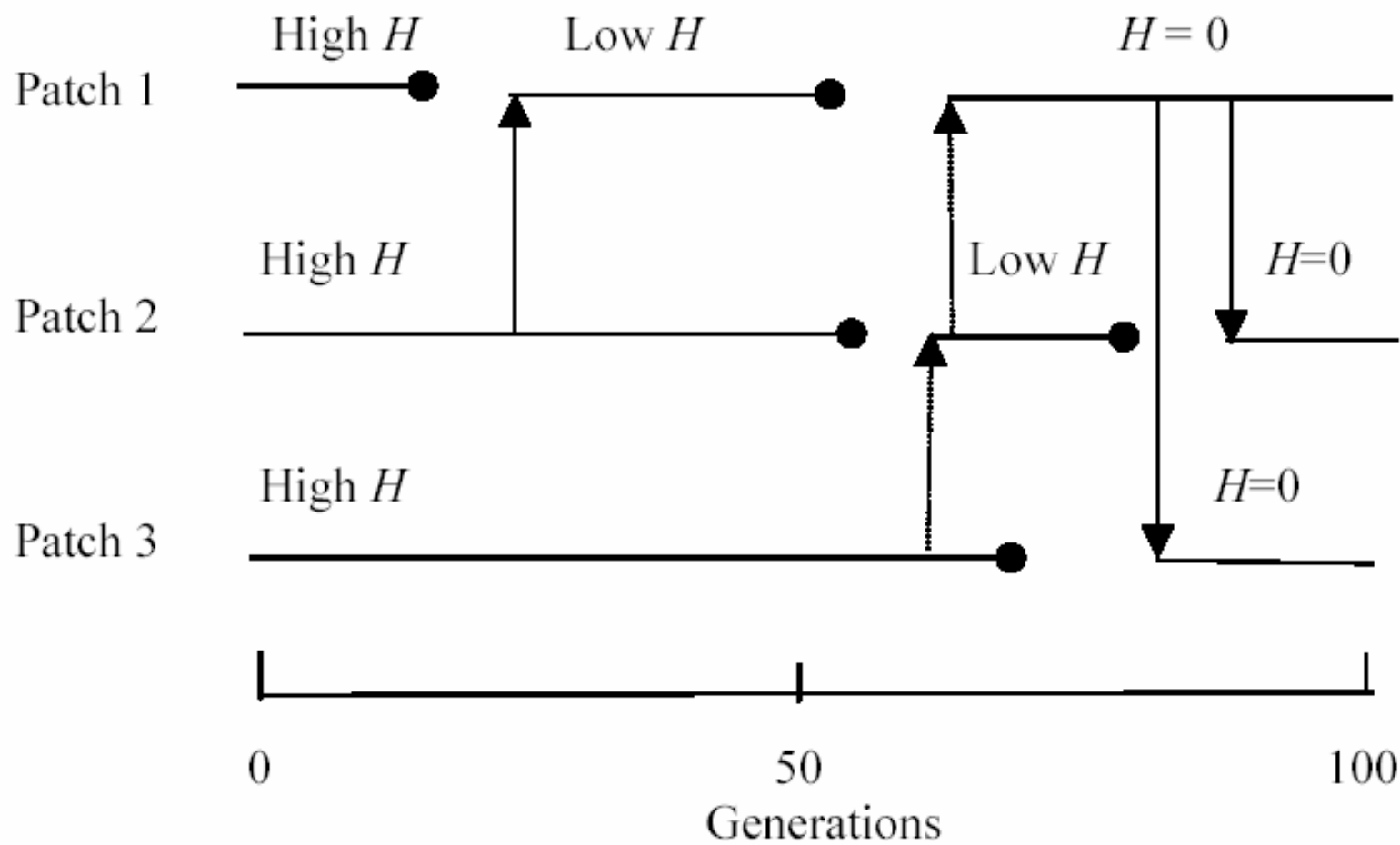
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It is the total assemblage of interconnected subpopulations that forms a global population that must have an effective size meeting the criteria for long-term persistence.



Effects of local extinctions



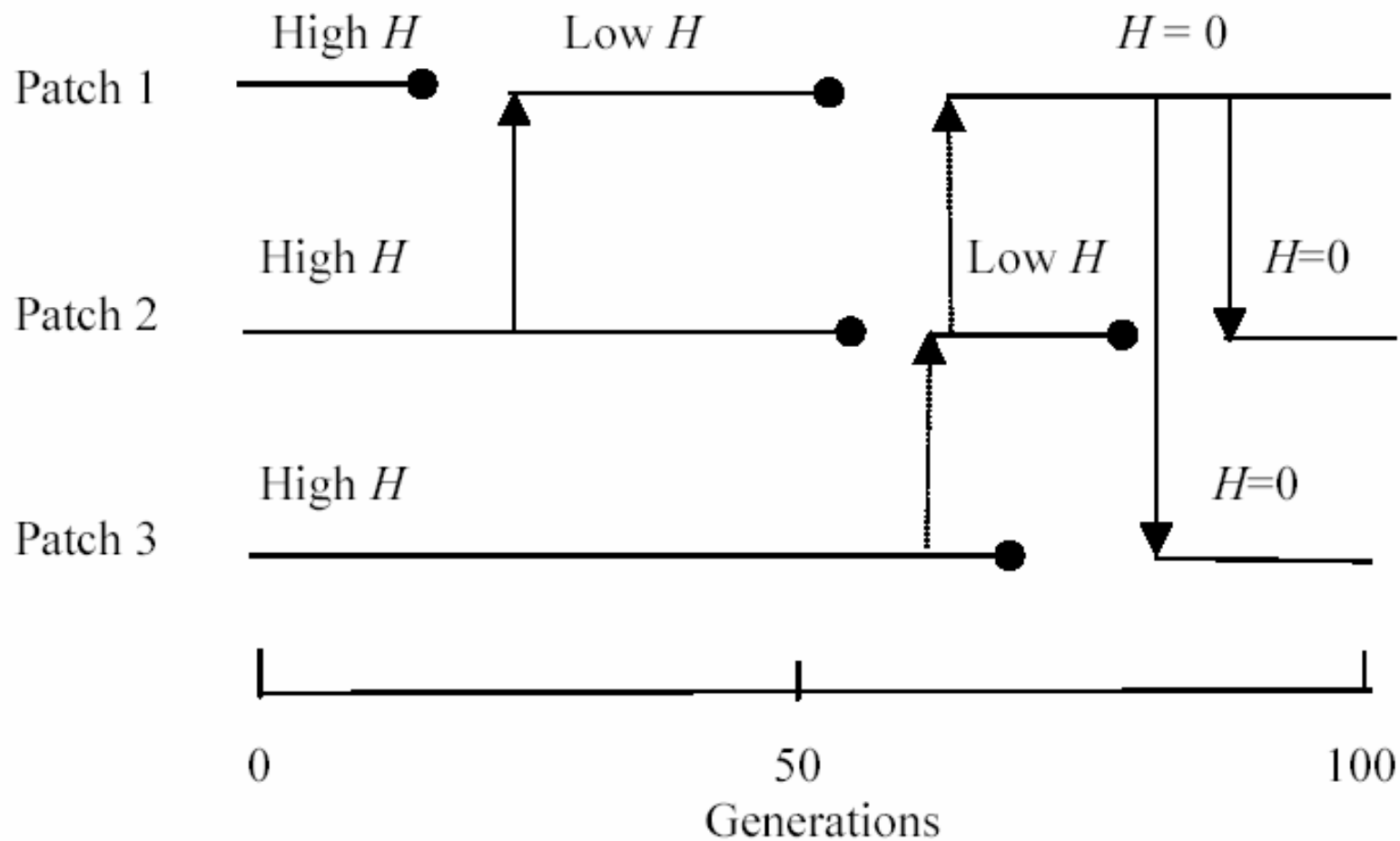
Few founders
from one patch



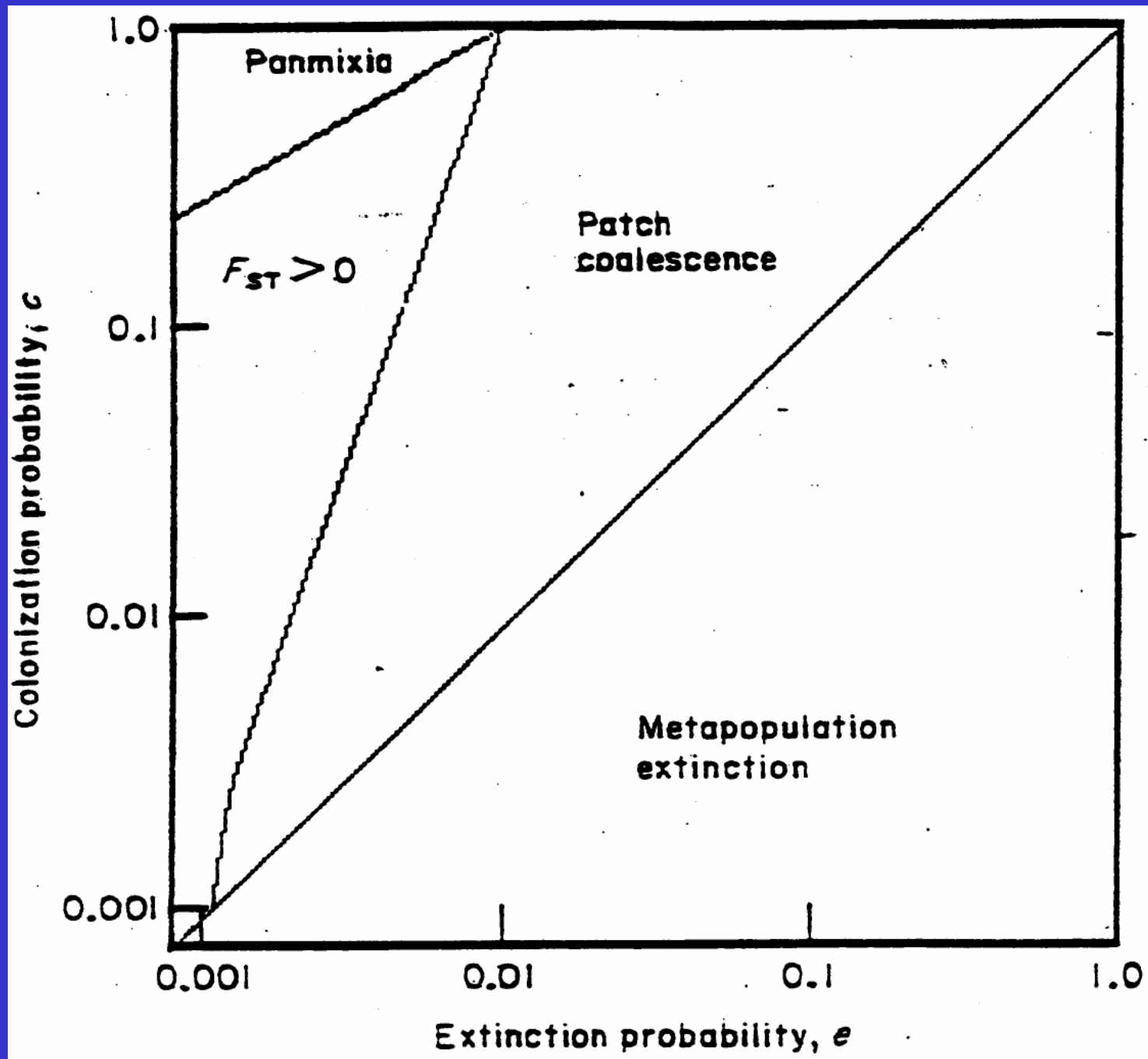
Many founders from
several patches

Greater F_{ST}

Smaller F_{ST}



Nuclear versus mtDNA?



?

Biocomplexity and fisheries sustainability

Ray Hilborn^{*†}, Thomas P. Quinn^{*}, Daniel E. Schindler[‡], and Donald E. Rogers^{*}

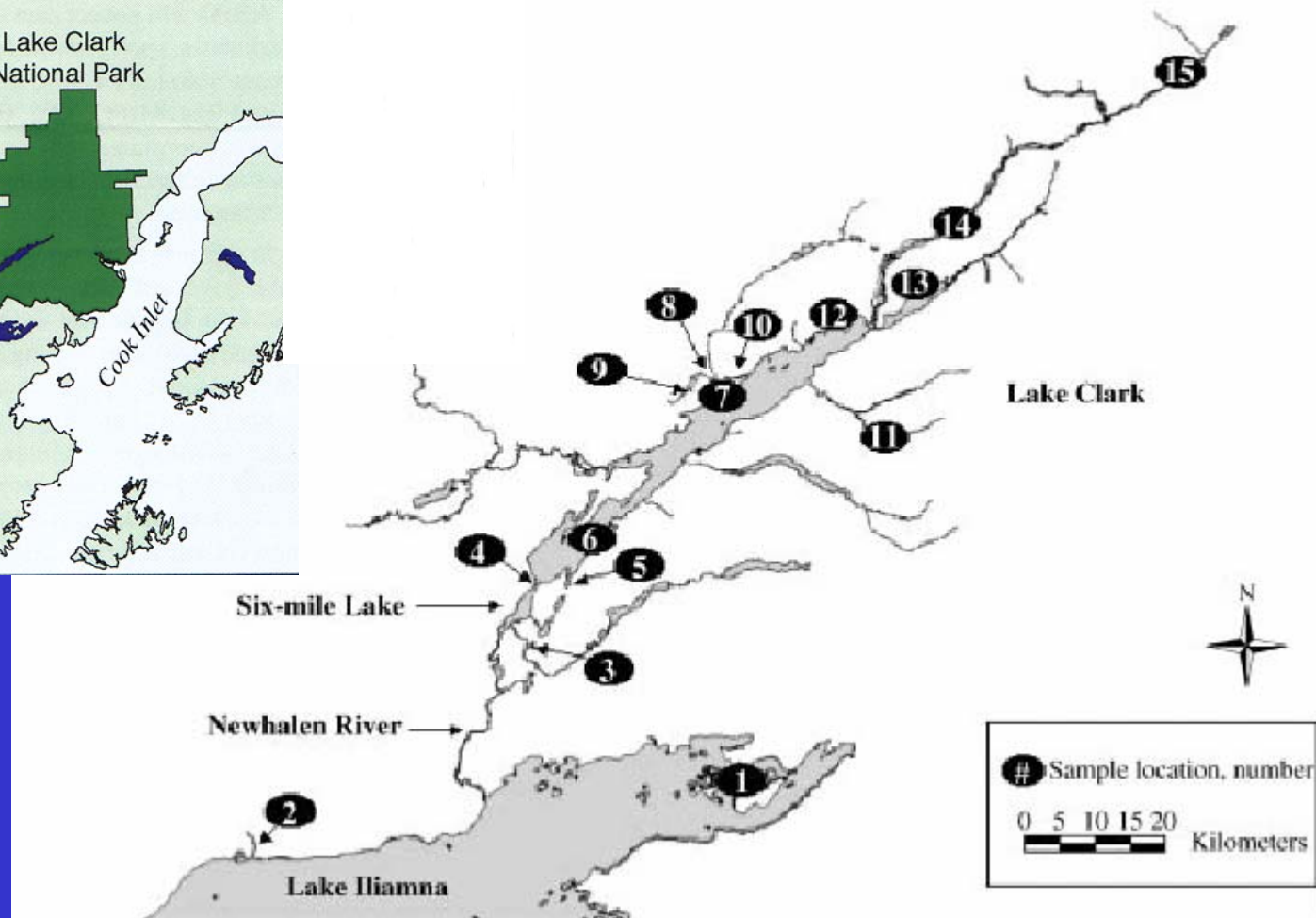
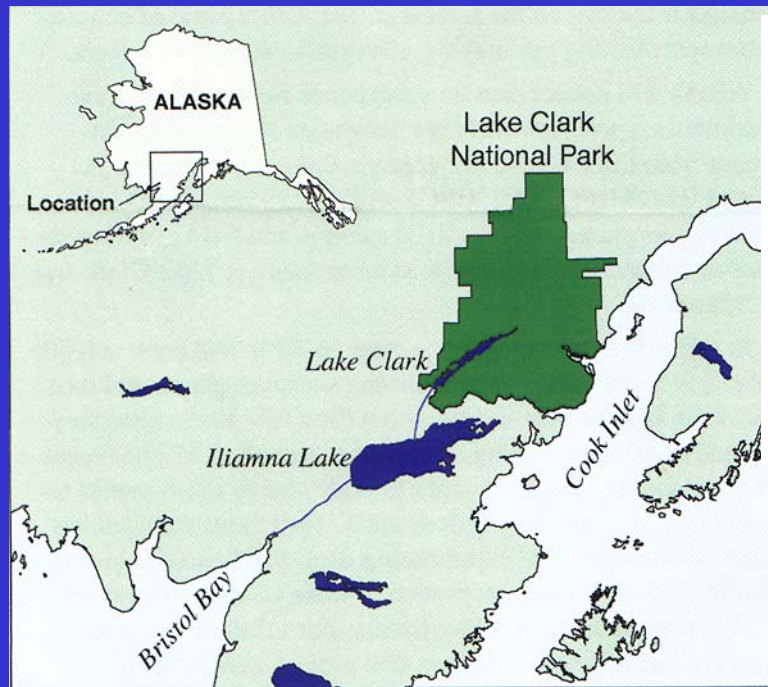
Proc. Nat. Acad. Sci. USA 100:6564-6568. 2003.

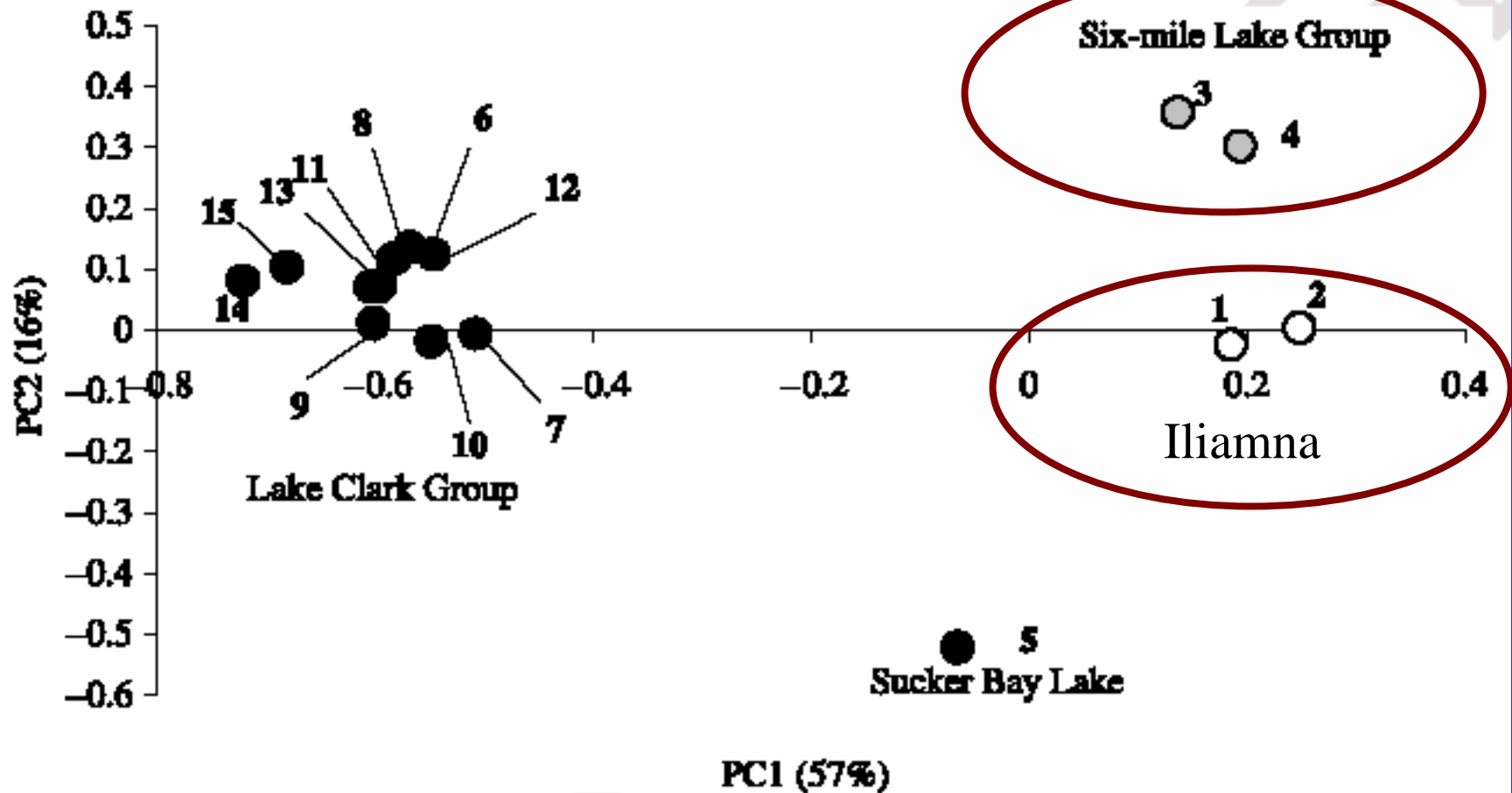
Table 1. A summary of life history variation within the Bristol Bay stock complex of sockeye salmon

| Element of biocomplexity | Range of traits or options found |
|---|---|
| Watershed location within Bristol Bay complex | Seven different major watersheds, ranging from maritime-influenced systems on the Alaskan Peninsula to more continental systems |
| Time of adult return to freshwater | June–September |
| Time of spawning | July–November |
| Spawning habitat | Major rivers, small streams, spring fed ponds, mainland beaches, island beaches |
| Body size and shape of adults | 130–190 mm body depth at 450 mm male length: sleek, fusiform to very deep-bodied, with exaggerated humps and jaws |
| Egg size | 88–116 mg at 450 mm female length |
| Energetic allocation within spawning period | Time between entry into spawning habitat and death ranges from 1–3 days to several weeks |
| Time spent rearing in freshwater | 0–3 years |
| Time spent at sea | 1–4 years |

Founding events influence genetic population structure of sockeye salmon (*Oncorhynchus nerka*) in Lake Clark, Alaska

K. M. RAMSTAD,* C. A. WOODY,† G. K. SAGE† and F. W. ALLENDORF*





Principle Component Analysis (PCA) of genetic divergence at 11 microsatellite loci



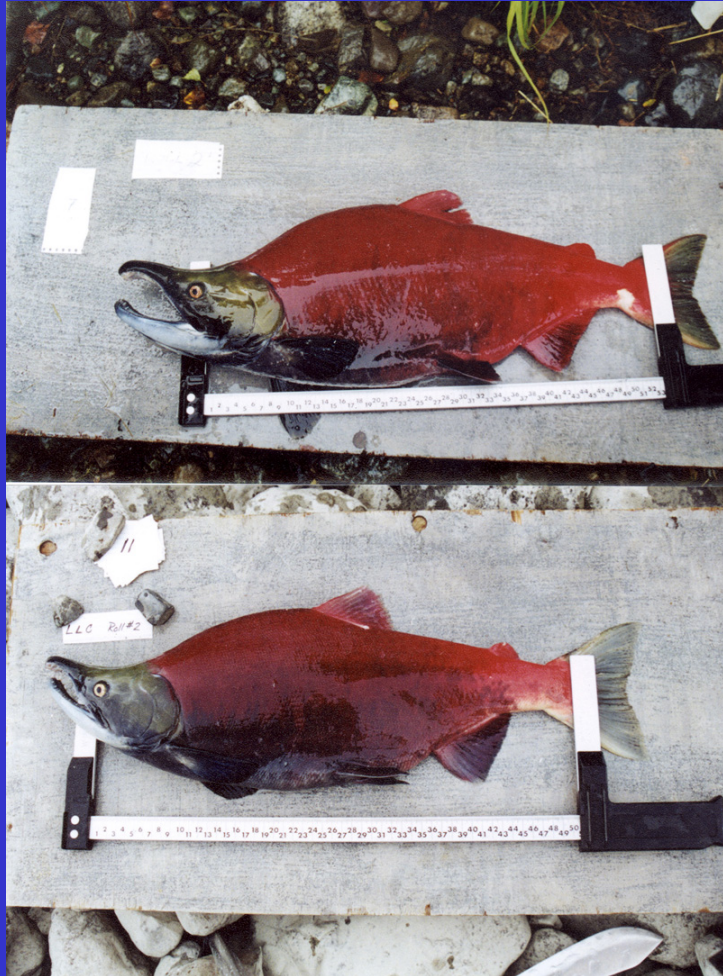


Stream spawners

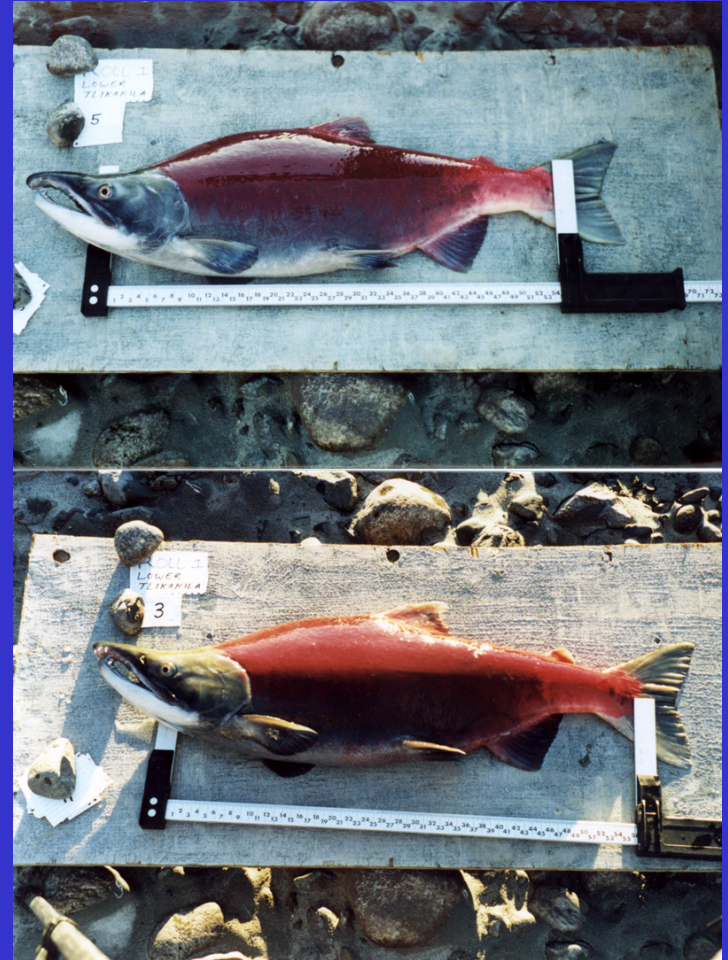


Beach
spawners

Local Adaptation



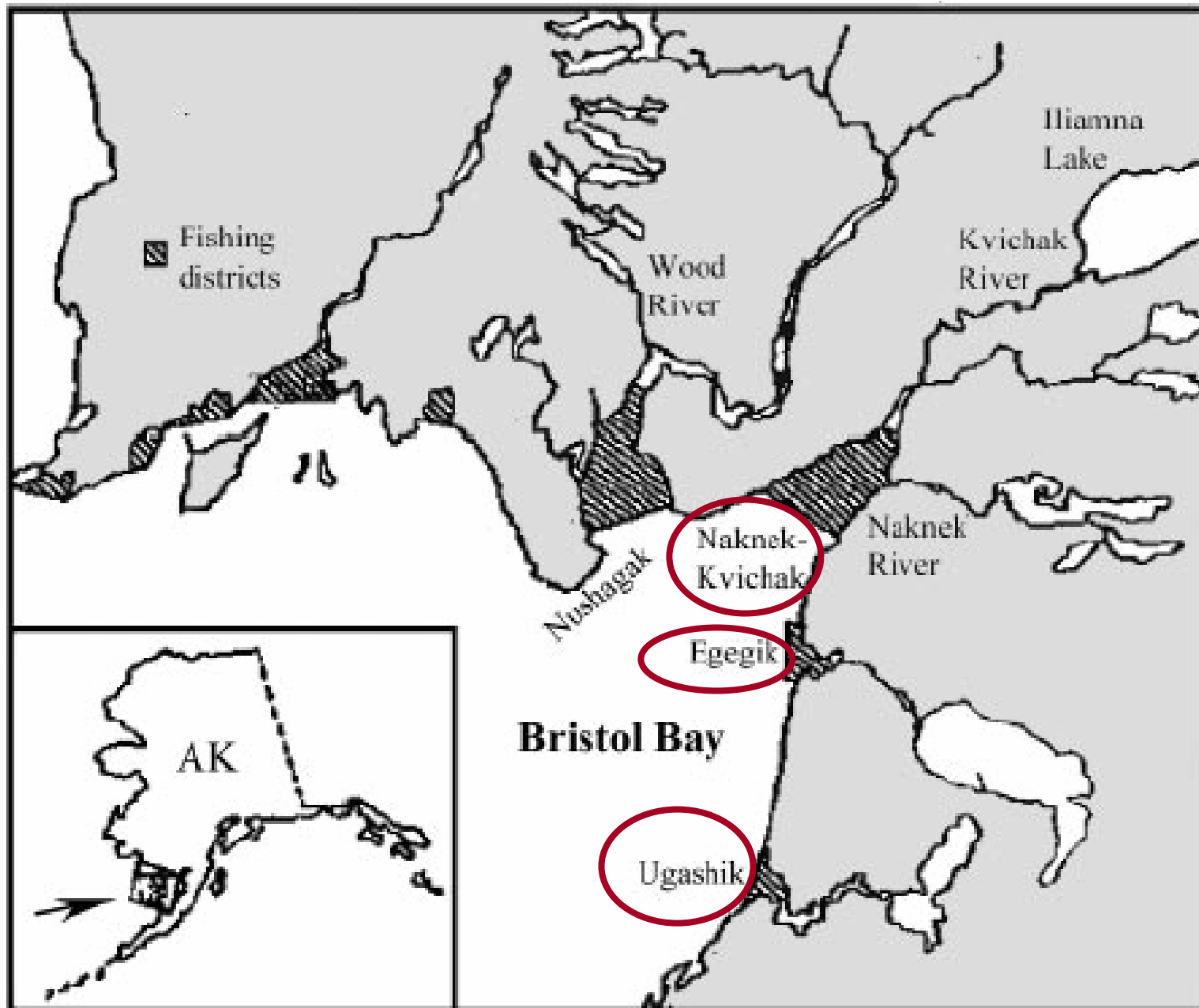
Beach spawners

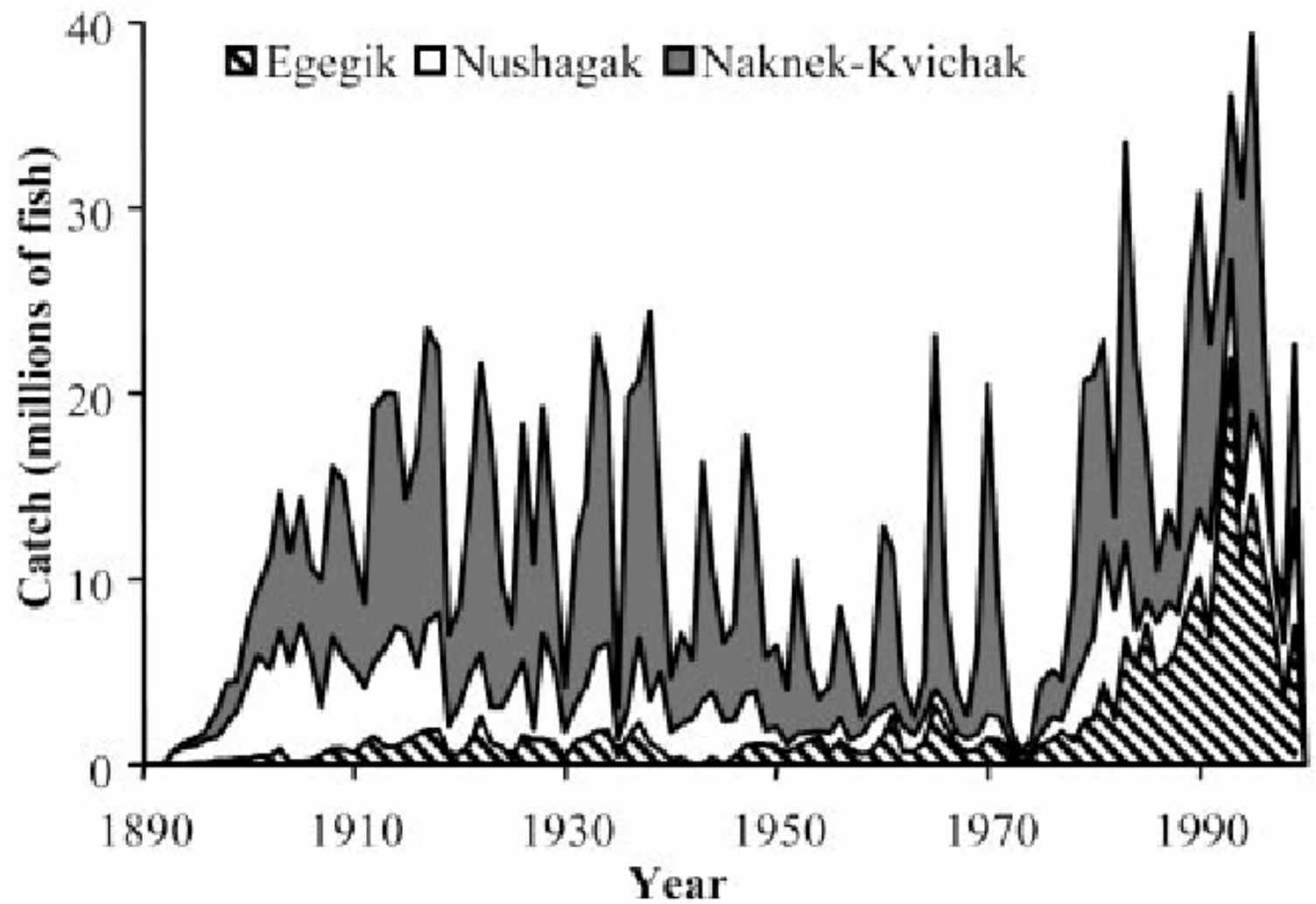


Stream spawners

The *stock complex* is an amalgamation of several hundred discrete spawning populations. Structured within lake systems, individual populations display diverse life history characteristics and local adaptations to the variation in spawning and rearing habitats. This biocomplexity has enabled the aggregate of populations to sustain its productivity despite major changes in climatic conditions affecting the freshwater and marine environments during the last century. Different geographic and life history components that were minor producers during one climatic regime have dominated during others, emphasizing that the biocomplexity of fish stocks is critical for maintaining their resilience to environmental change.

Hilborn et al. (2003)





CHAPTER 16

UNITS OF CONSERVATION

The choices of what to conserve must often be made with regard to populations that are not separate completely from others, or when information regarding the relationships and degrees of distinction among populations is very incomplete.

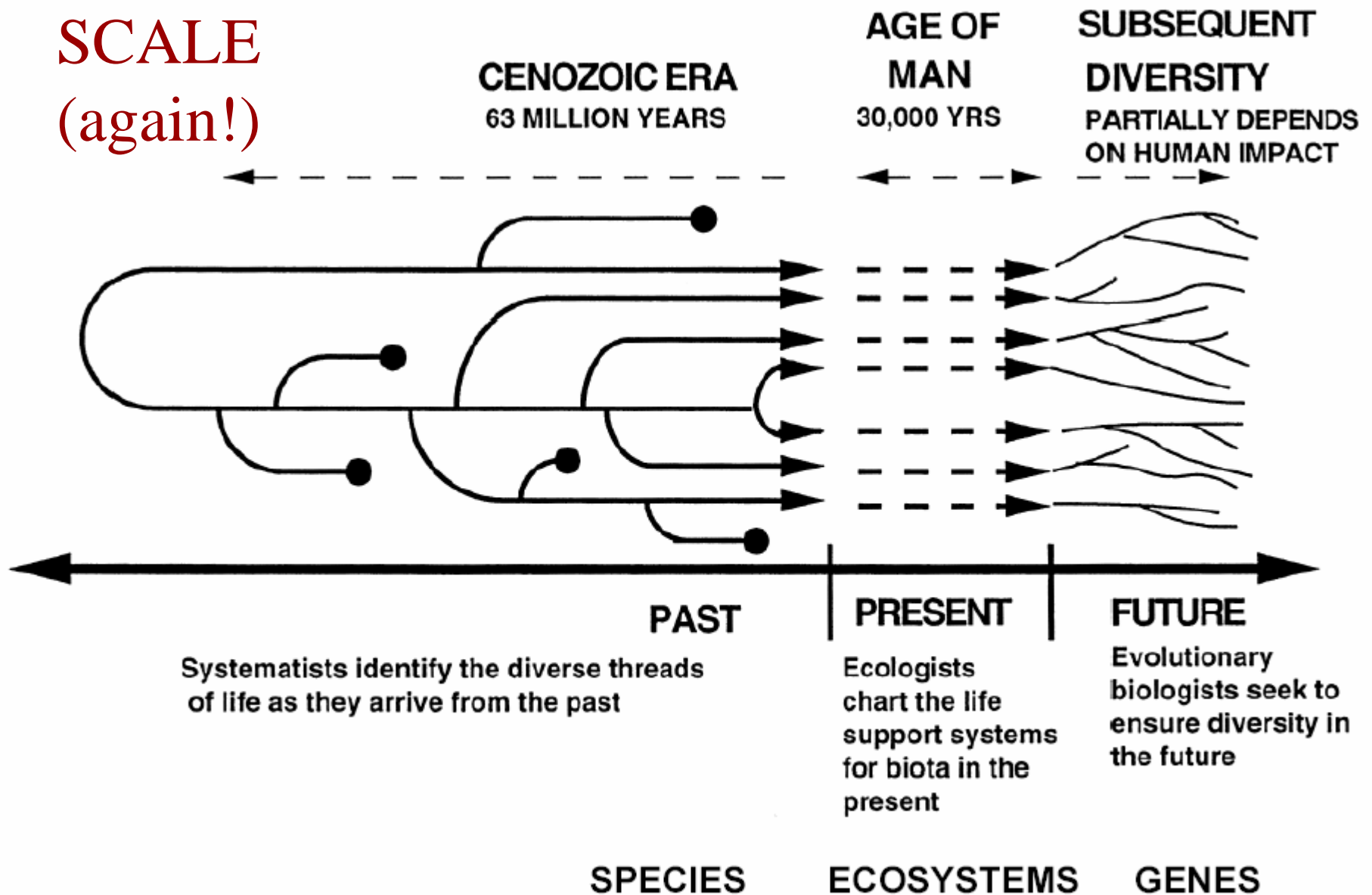
Jody Hey et al. (2003)

What are we trying to “conserve”?

Recognizing appropriate intraspecific units for protection and management is essential:

- (1) Management and monitoring need to be targeted at independent populations.
- (2) Many governments and agencies have established legislation and policies to protect intraspecific population units.
- (3) Priorities among population units are often needed because limited financial resources preclude conservation of all units.

SCALE
(again!)



Great Fundamental Ignorance

How many species of animals are there? 6 million or 35 million?



African Savannah



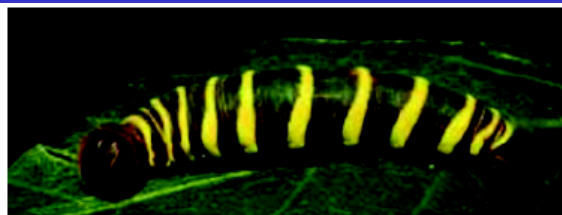
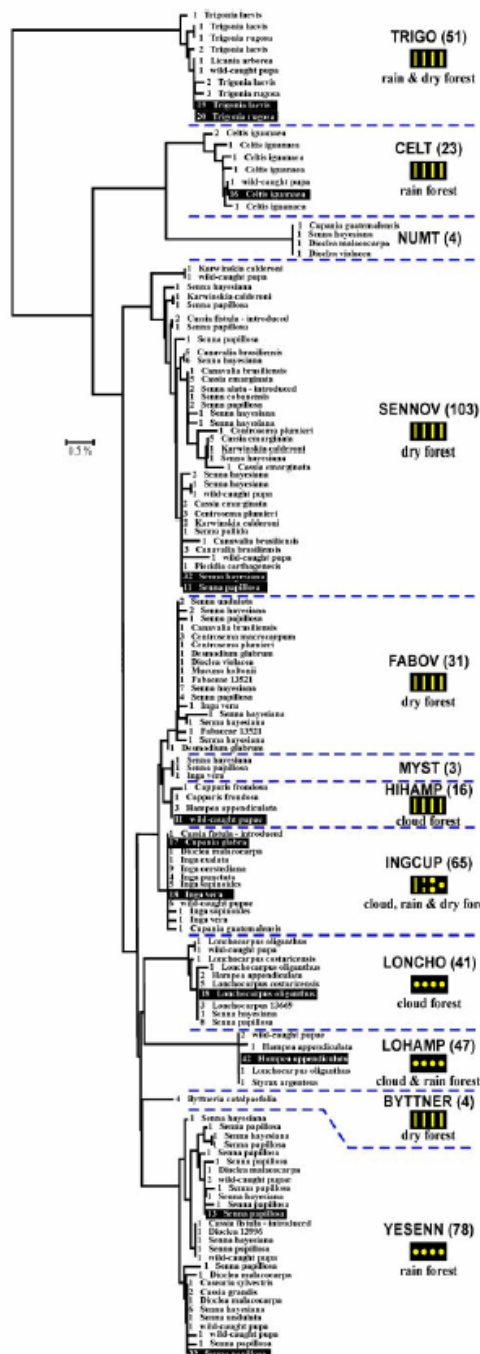
African Forest

Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astraptes fulgerator*

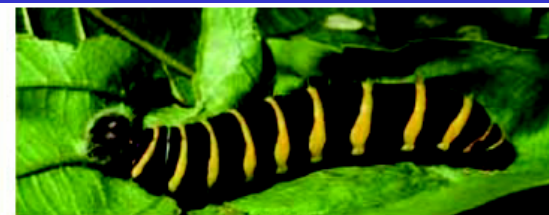
Paul D. N. Hebert^{*†}, Erin H. Penton^{*}, John M. Burns[‡], Daniel H. Janzen[§], and Winnie Hallwachs[§]

2004. PNAS 101:14812-14817.





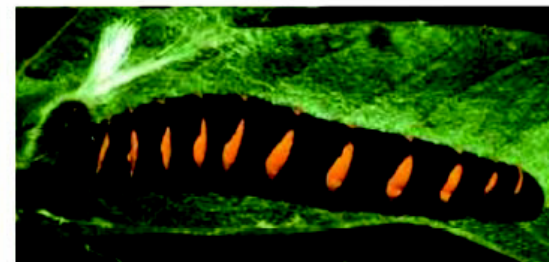
TRIGO



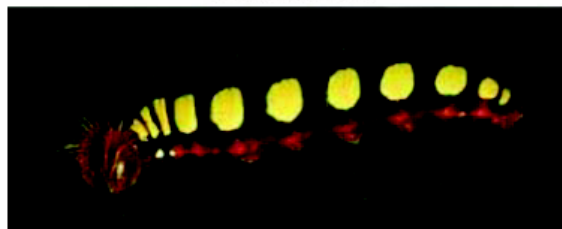
CELT



LONCHO



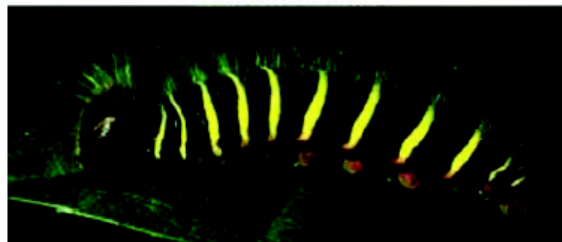
INGCUP



LOHAMP



HIHAMP



BYTTNER



FABOV

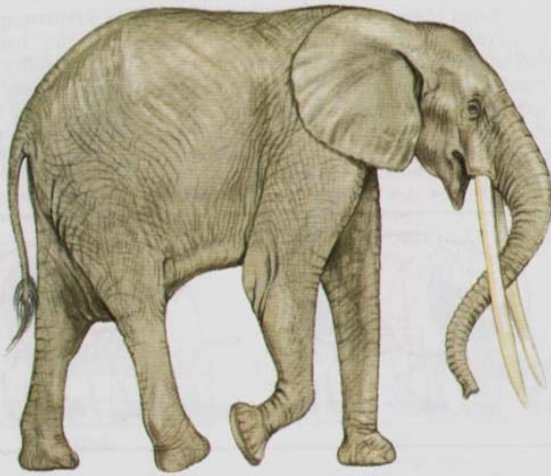


YESENN



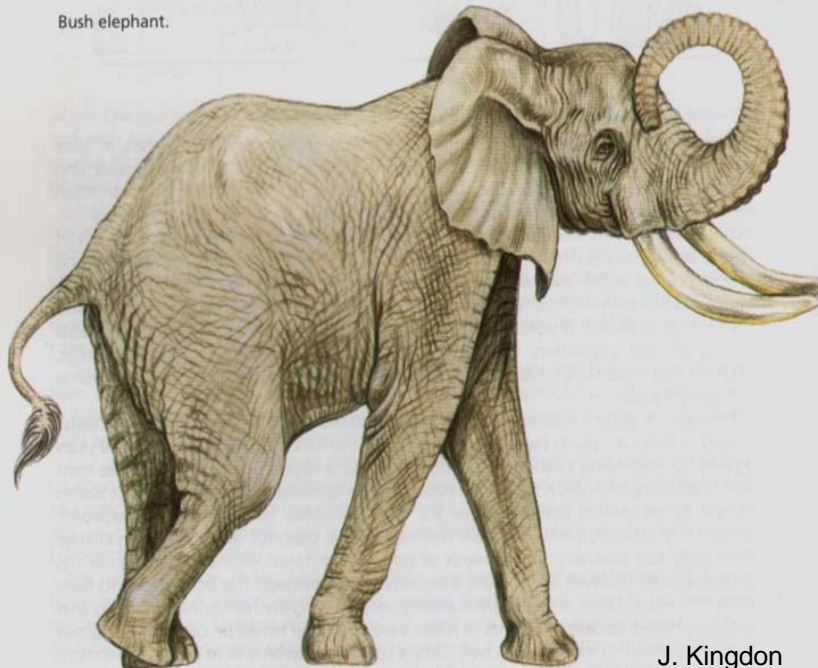
SENNOV

Forest elephant.

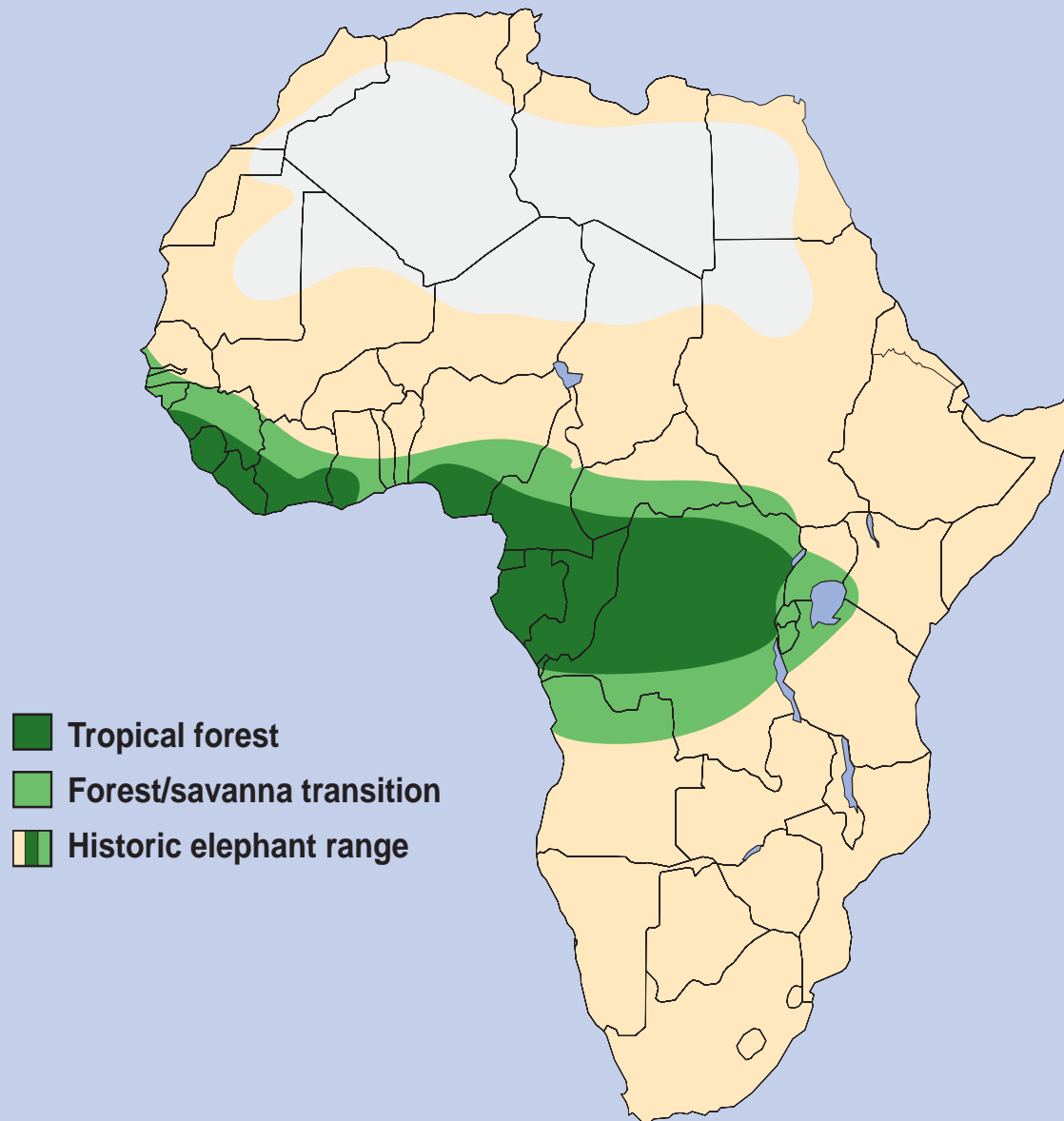


Forest elephant

Bush elephant.

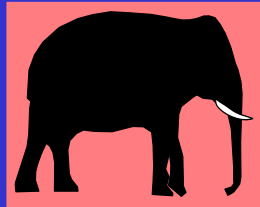


Savannah elephant

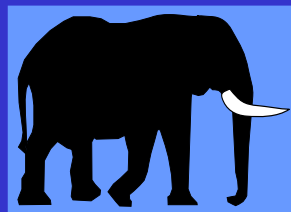


BGN
haplotypes
646 bp

Asian



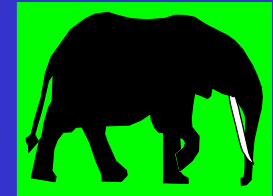
EMA1
n=13



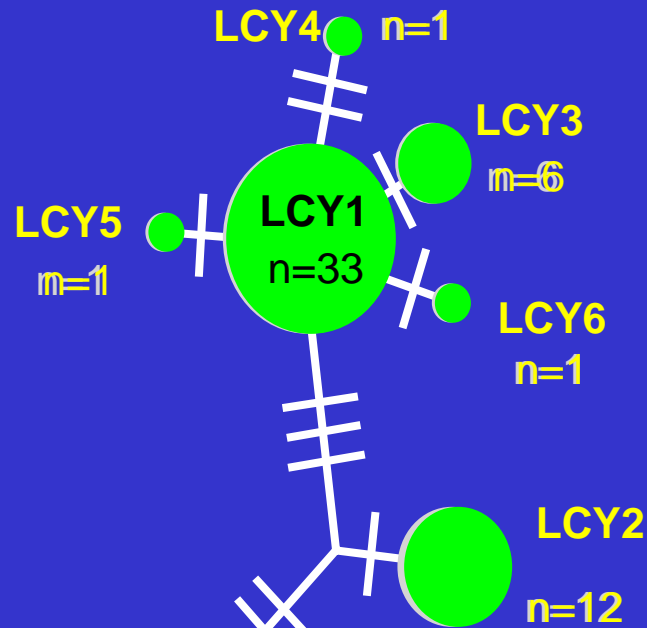
LAF2
n=2

LAF1
n=101

African
Forest



African
Savannah





NJ Tree
1732 bp
4 nuclear
genes

African Forest Elephants: Dzangha-Sangha Lope Odzala

Cameroon
Eastern Africa
Southern Africa
Namibia

16 microsatellite loci

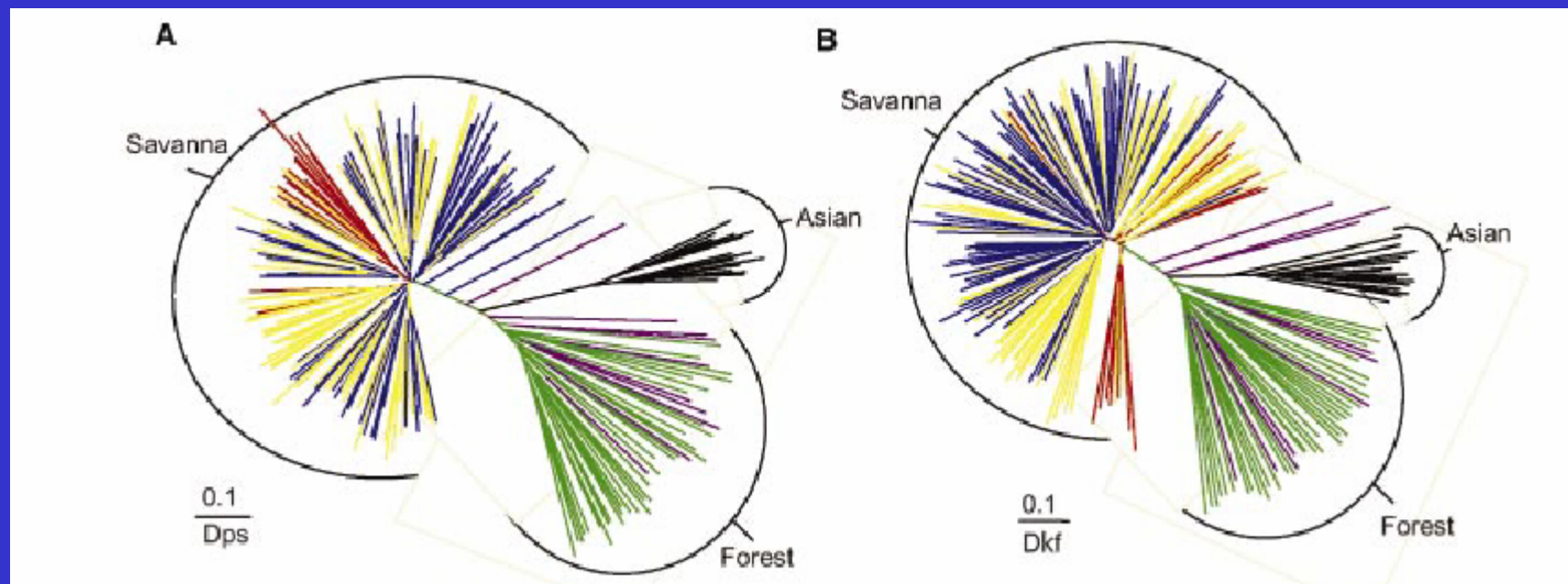
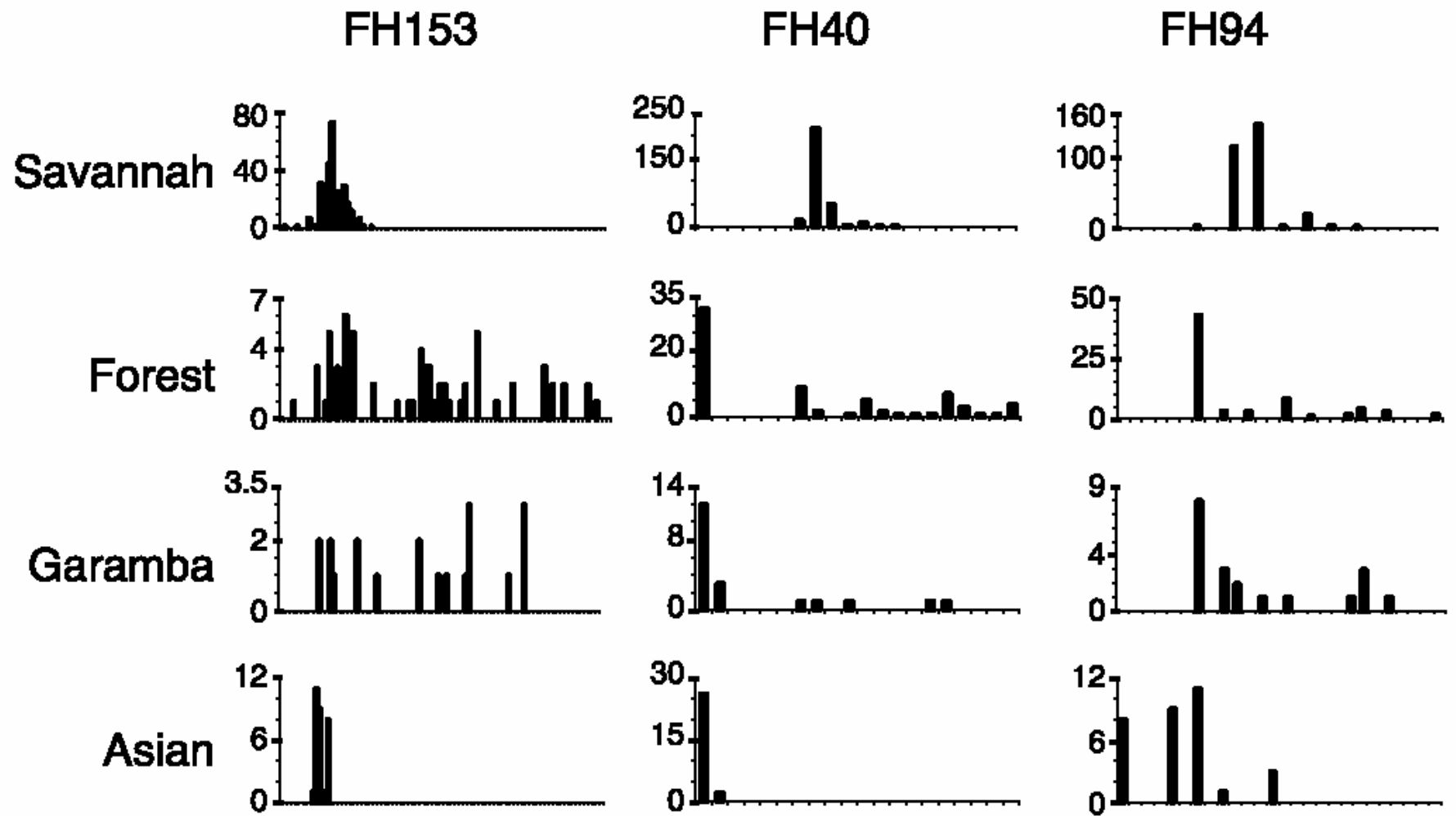
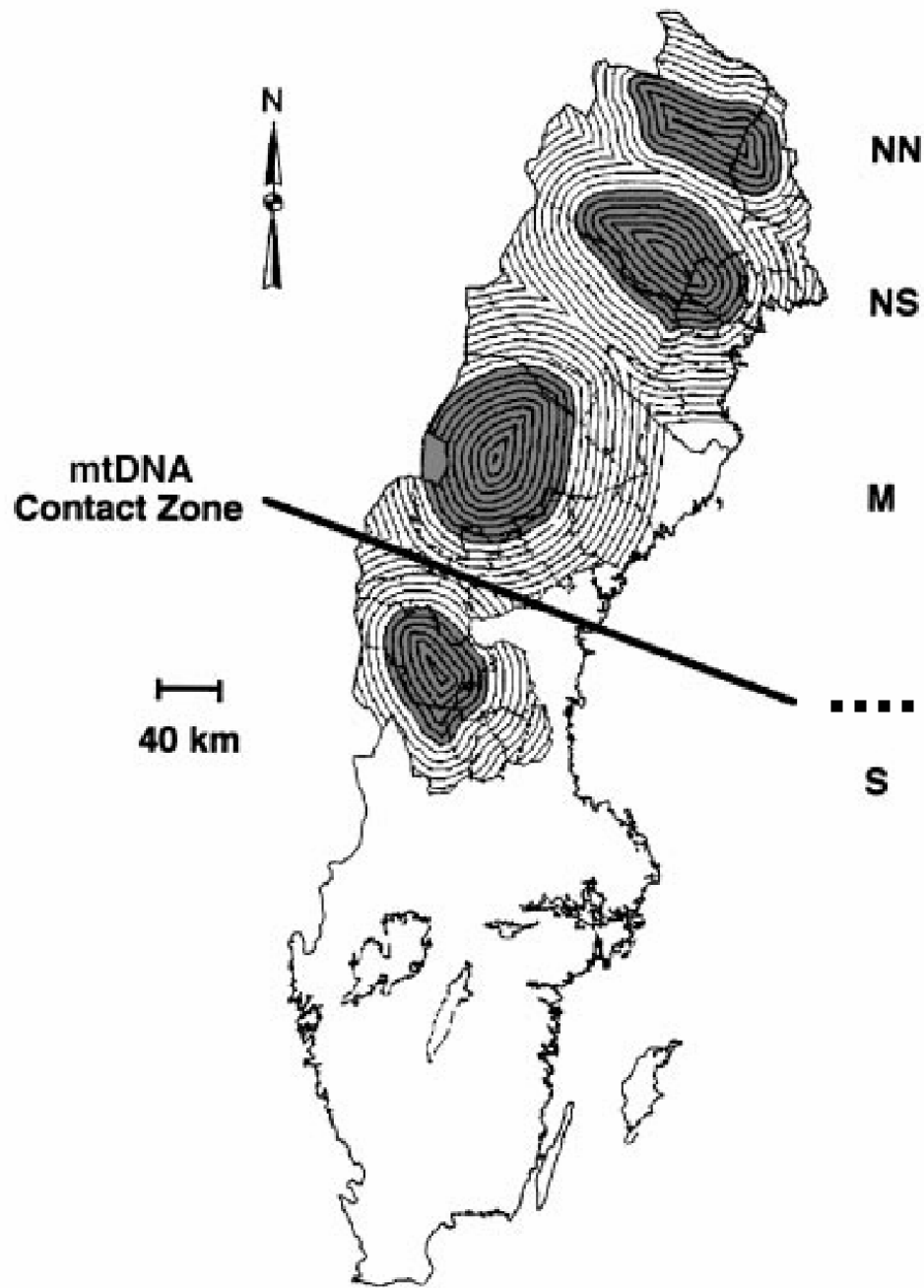


Table 1B Measures of genetic variation across 16 microsatellite loci in different phylogeographical groups of elephants

| Phylogeographical group | Locales | No. Ind. | Ave. H_O (\pm SE) | No. alleles | | Ave. no. alleles/locus | Ave. range* (bp) |
|-------------------------|----------------------------------|----------|------------------------|-------------|---------------|------------------------|------------------|
| | | | | Total | Pop. Specific | | |
| Asian (14/16 loci) | Asia | 14 | 0.56 ± 0.30 | 56 | 15 | 4.3 | 9.7 |
| African | Forest, Savannah | 189 | 0.64 ± 0.14 | 271 | 134 | 16.5 | 44.8 |
| Forest | DS, LO, GR | 42 | 0.77 ± 0.11 | 221 | 114 | 13.8 | 41.0 |
| Savannah | North-central, Eastern, Southern | 147 | 0.60 ± 0.17 | 161 | 30 | 9.3 | 21.9 |
| North-central | BE, WA | 15 | 0.58 ± 0.12 | 82 | 1 | 5.1 | 13.6 |
| Eastern | AB, AM, KE, MK, NG, SE, TA | 60 | 0.61 ± 0.17 | 125 | 9 | 8.1 | 18.0 |
| Southern | CH, HW, KR, MA, NA, SA, SW, ZZ | 72 | 0.61 ± 0.18 | 137 | 10 | 8.3 | 18.0 |



How much of this genetic variation is present in captive populations of elephants?



mtDNA
suggested
subspecies

$$F_{ST} \sim 1.0$$

$$mN = 0$$